

## (1) GENERAL INFORMATION:



- (i) APPLICANTS: Gaugler, Béatrice; Van den Eynde, Benoît;  
van der Bruggen, Pierre; Boon-Falleur, Thierry
- (ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Felfe & Lynch  
(B) STREET: 805 Third Avenue  
(C) CITY: New York City  
(D) STATE: New York  
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
(B) COMPUTER: IBM  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/037,230  
(B) FILING DATE: 26-MARCH-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/US92/04354  
(B) FILING DATE: 22-MAY-1992
- (viii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/807,043  
(B) FILING DATE: 12-DECEMBER-1991
- (ix) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/764,364  
(B) FILING DATE: 23-SEPTEMBER-1991
- (x) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/728,838  
(b) FILING DATE: 9-JULY-1991
- (xi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/705,702  
(B) FILING DATE: 23-MAY-1991
- (xii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Hanson, Norman D.  
(B) REGISTRATION NUMBER: 30,946  
(C) REFERENCE/DOCKET NUMBER: LUD 253.5
- (xiii) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 688-9200  
(B) TELEFAX: (212) 838-3884

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- (2) INFORMATION FOR SEQUENCE ID NO: 1:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 462 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60  
 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120  
 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTCGA AGTTCCGCCT ACAGCTCTAG 180  
 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240  
 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300  
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT 360  
 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420  
 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

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 5.1

- (2) INFORMATION FOR SEQUENCE ID NO: 2:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 675 base pairs  
 (B) TYPE: nucleic acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48  
 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly  
 5 10 15  
 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96  
 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu  
 20 25 30  
 GAA ATT CTG CTT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144  
 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr  
 35 40 45  
 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192  
 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln  
 50 55 60  
 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240  
 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser  
 65 70 75 80  
 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288  
 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr  
 85 90 95  
 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336  
 Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp  
 100 105 110  
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384  
 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu  
 115 120 125  
 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432  
 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met  
 130 135 140  
 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480  
 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys  
 145 150 155 160  
 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528  
 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe  
 165 170 175  
 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576  
 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys  
 180 185 190  
 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG 624  
 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu  
 195 200 210  
 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672  
 Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro  
 220 225 230 235  
 TAG 675

## (2) INFORMATION FOR SEQUENCE ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
(B) TYPE: nucleic acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60  
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120  
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC 180  
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228

- (2) INFORMATION FOR SEQUENCE ID NO: 4:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 1365 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50  
 GAAGATCGTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100  
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150  
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200  
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250  
 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300  
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350  
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400  
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450  
 ACCCTTTGTG CC 462  
 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504  
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546  
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588  
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630  
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672  
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714  
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756  
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798  
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840  
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882  
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924  
 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966  
 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008  
 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050  
 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092  
 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134  
 TAG 1137  
 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187  
 TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237  
 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287  
 CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGATCCT 1337  
 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

- (2) INFORMATION FOR SEQUENCE ID NO: 5:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 4698 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	50
GAAGATCTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	100
CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTTT	GCTCTCCCG	350
CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCTGAAG	AAGTAAGCCG	400
CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG	CC				462
ATG TCT GAT	AAC AAG AAA CCA	GAC AAA GCC CAC	AGT GGC TCA		504
GGT GGT GAC	GGT GAT GGG AAT	AGG TGC AAT TTA	TTG CAC CGG		546
TAC TCC CTG	GAA GAA ATT CTG	CCT TAT CTA GGG	TGG CTG GTC		588
TTC GCT GTT	GTC ACA ACA AGT	TTT CTG GCG CTC	CAG ATG TTC		630
ATA GAC GCC	CTT TAT GAG GAG	CAG TAT GAA AGG	GAT GTG GCC		672
TGG ATA GCC	AGG CAA AGC AAG	CGC ATG TCC TCT	GTC GAT GAG		714
GAT GAA GAC	GAT GAG GAT GAT	GAG GAT GAC TAC	TAC GAC GAC		756
GAG GAC GAC	GAC GAC GAT GCC	TTC TAT GAT GAT	GAG GAT GAT		798
GAG GAA GAA	GAA TTT GAG AAC	CTG ATG GAT GAT	GAA TCA GAA		840
GAT GAG GCC	GAA GAA GAG ATG	AGC GTG GAA ATG	GGT GCC GGA		882
GCT GAG GAA	ATG GGT GCT GGC	GCT AAC TGT GCC	T		916
GTGAGTAACC	CGTGGTCTTT	ACTCTAGATT	CAGGTGGGGT	GCATTCTTTA	966
CTCTTGCCCC	CATCTGTAGT	AAAGACCACA	TTTGGTTGG	GGGTCATTGC	1016
TGGAGCCATT	CCTGGCTCTC	CTGTCCACGC	CTATCCCCGC	TCCTCCCATC	1066
CCCCACTCCT	TGCTCCGCTC	TCCTTCTTTT	TCCCACCTTG	CCTCTGGAGC	1116
TTCAGTCCAT	CCTGCTCTGC	TCCCTTCTCC	CTTGCTCTC	CTTGCTCCCC	1166
TCCCCCTCGG	CTCAACTTTT	CGTCCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
TTCAGGCTTC	CCCATTGCT	CCTCTCCCGA	AACCCTCCCC	TTCCTGTTCC	1266
CCTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTC	CCCTTTTGCA	CCTTTTCTTT	1366
TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416
CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTTG	CATTTTCGGG	1466
TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCGGGTGCT	1516
CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCTGGCAC	1616
TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	GAGAAATCTG	CCTGCCTCTG	1666
CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
AACTCCCTTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTAGCTCTC	CCTGCTTTCT	1916
GCCCCGTTCC	CCTTTTTTGT	GCCTTTCTCT	CTGGCTCCCC	TCCACCTTCC	1966
AGCTCACCTT	TTTGTTTGTT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCTCCCCC	TCCGGCTTCC	2066
CCTCTGTGTG	CCTTTCTCTG	TCCCTCCCCC	TCGCTGGGTC	CCCCTCCCTT	2116
TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
CTTTTCTAGA	CTCCCCCTTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
CCTGACCCTG	CTCCCTTCC	CCTCCAGCT	CCCCCTCTTT	TTCCACCTC	2266
CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
GACTTCCTCT	CCAGCCGCCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCTT	2466
ATGTGTCTCT	CTTCTATCT	ATCCCTTCC	TTCTGTCCCC	TCTCTCTGT	2516
CCATCACCTC	TCTCCTCCCT	TCCCTTTTCT	CTCTCTTCCA	TTTTCTTCCA	2566
CCTGCTTCTT	TACCCTGCCT	CTCCCATTC	CCTCTTACCT	TTATGCCCAT	2616
TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666

ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC 2716  
 TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCTATG CCCTCTACTC 2766  
 TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC 2816  
 CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC 2866  
 ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCCAA ATCAGCAGGA 2916  
 AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC 2966  
 AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT 3016  
 CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG 3066  
 CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA 3116  
 GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG 3166  
 TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA 3216  
 TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTAA 3266  
 GGCTAAAGAT ACTTGAACCC ATAGAAGCGT TGTAAAATA CTGCTTTCTT 3316  
 TTGCTAAAAT ATTCTTTCTC ACATATTTCAT ATTCTCCAG 3355  
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT 3396  
 AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT 3438  
 ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA 3480  
 AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA 3522  
 GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC 3564  
 TTC TCA CCT TAG 3576  
 GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA 3626  
 GCTAAGAGCA TCTTTTAAA AATATTATT GGTAAACTAA ACAATTGTGA 3676  
 TCTTTTACA TTAATAAGTA TTAATTAAAT CCAGTATACA GTTTTAAGAA 3726  
 CCCTAAGTTA AACAGAAAGT AATGATGTCT AGATGCCTGT TCTTTAGATT 3776  
 GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA 3826  
 GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG 3876  
 TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT 3926  
 TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCTG 3976  
 TTCTGATTTT TTTCATTCTT AGACCTGTGG TTTTAAAGAG ATGAAAATCT 4026  
 CTTAAAATTT CCTTCATCTT TAATTTTCTT TAACTTTAGT TTTTTCCTACT 4076  
 TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTAA GATTTCTTAA 4126  
 AATGTTTTTT AAAAAAATG CAAATCTCAT TTTTAAAGAGA TGAAAGCAGA 4176  
 GTAAGTGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA 4226  
 GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAACC AGGCCCTTGC 4276  
 CAGTAGGTTA GTGAGGTGA TATGATCAGA TTATGGACAC TCTCCAATC 4326  
 ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT 4376  
 ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA 4426  
 AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTCTTAT TTCTTCTAC 4476  
 AGTTGCAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT 4526  
 TTTTTCCTC TTCATTAAAT TTCTAGTTT TAGTAATCCA GAAATTTGA 4576  
 TTTTGTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT 4626  
 GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTAAA 4676  
 AATAAAGTT TGACTTGCAT AC 4698

- (2) INFORMATION FOR SEQUENCE ID NO: 6:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 9 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe  
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- (2) INFORMATION FOR SEQUENCE ID NO: 7:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 2418 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG 50  
 GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC 100  
 TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG 150  
 GGCCCGTGGA TTCTCTTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT 200  
 TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT 250  
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300  
 CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT 350  
 CCTGTAGAAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC 400  
 TTCCTCCTTC AGGTTTTTCAG GGGACAGGCC AACCAGAGG ACAGGATTCC 450  
 CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG 500  
 TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTCTCA CACTCTCCCT 550  
 CTCTCCCCAG GCCTGTGGGT CTTTATTGCC CAGCTCCTGC CCACACTCCT 600  
 GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC 650  
 ACTGCAAGCC TGAGGAAGCC CTTGAGGCCA AACAAGAGGC CCTGGGCCTG 700  
 GTGTGTGTGC AGGCTGCCAC CTCTCTCTCC TCTCCTCTGG TCCTGGGCAC 750  
 CCTGGAGGAG GTGCCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC 800  
 AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA 850  
 CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG 900  
 TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT 950  
 TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG 1000  
 GCAGAAATGC TGGAGAGTGT CATCAAAAT TACAAGCACT GTTTTCCTGA 1050  
 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100  
 TGAAGGAAGC AGACCCACCC GGCCACTCCT ATGTCTTGT CACCTGCCTA 1150  
 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200  
 AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GCGCGCCATG 1250  
 CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300  
 GGGAGGGGAG ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350  
 TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCCG ACAGTGATCC 1400  
 CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450  
 ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAAGTGAAG AGTTCGCTTT 1500  
 TTCTTCCCAT CCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550  
 CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600  
 ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG 1650  
 CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTCTCTAGT AGTAGGTTTC 1700  
 TGTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT 1750  
 TCAAATGTTT TTTTTTAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT 1800  
 TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA 1850  
 GTCTTGTTGT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG 1900  
 ATAATAACAG CAGTGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA 1950  
 AAATAGATGA GATAAAGAAC TAAAGAAAT AAGAGATAGT CAATTCTTGC 2000  
 CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG 2050  
 GATTTCTCTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100  
 AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC 2150  
 TTTTGGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200  
 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250  
 AGGTGGCAAG ATGTCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300  
 GGGTGTGGGG CTCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG 2350  
 GGCAATTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT 2400  
 AATGATCTTG GGTGGATCC 2418

- (2) INFORMATION FOR SEQUENCE ID NO: 8:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5724 base pairs
- (B) TYPE: nucleic acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-1 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCCGGGGCACC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT 50

TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCCAGCC CAAGCCAGGC 100

AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCAG 150

ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200

CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGGAAGCGG CCCAGCTCTG 250

TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300

AGATAGAGGA CCCAAAATAA TCCCTTCATG CCAGTCTTGG ACCATCTGGT 350

GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA 400

CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGGAAG GCTGCTTAGG 450

AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAG 500

AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550

ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCTATT CCAACCCCCA 600

CCCCACATCC CCCCACCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC 650

ATTCCACCCT CACCCCCACC CCCCACCCCA CGCCCCTCC CACCCCCACC 700

CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750

GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG 800

AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG 850

AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA 900

GAGAGCCCCA AATATTCCAG CCGCGCCCTT GCTGCCAGCC CTGGCCCCACC 950

CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCTT GCTCCAAAAG 1000

CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC 1050

TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA 1100

GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC 1150

ACTCCAATCC CCACTCCAC CCCATTGCA TTCCCATTC CCACCCAACC 1200

CCCATCTCCT CAGCTACACC TCCACCCCA TCCCTACTCC TACTCCGTCA 1250

CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACCC TTCTGCCACC 1300

TCACCCTCAC TGCCCCAAC CCCCACCTCA TCTCTCTCAT GTGCCCCACT 1350

CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTGTTGCCCC TGCTCTCAAC 1400

CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC 1450

AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG 1500

ATCCAATGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG 1550

CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCAAAATG 1600

ATCCAGTACC ACCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT 1650

GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG 1700

GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTCAGGAGA 1750

GGCAGGGCCC AGGCATCAAG GTCCAGCATC CGCCCCGCAT TAGGGTCAGG 1800

ACCCTGGGAG GGAAGTGAAG GTTCCCCACC CACACCTGTC TCCTCATCTC 1850

CACCGCCACC CCACTCACAT TCCCATACTT ACCCCCTACC CCAACCTCA 1900

TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC 1950

CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG 2000

GCTTGAACAG GGCCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA 2050

GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG 2100

ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA 2150

TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA 2200

GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT 2250

GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT CCTGCATCTT 2300

TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC 2350

AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG 2400

AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG 2450

CTGTCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA TGGCGGTATG 2500

TTCCATTCTC ACTTGTAACA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG 2550

ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGAAATTGG 2600

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AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTCAGC CCTGGACACC 2700

TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTCACAGA TCTGGGGCAG 2750  
 GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA GGGACCCCCA 2800  
 TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG 2850  
 GAACATGAGG GAGGACTGAG GGTACCCAGG GACCAGAACA CTGAGGGAGA 2900  
 CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCACAGAG AGCATGGGCT 2950  
 GGGCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT GATGTCAGGG 3000  
 ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG TAGAGGGAGC 3050  
 GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCACC 3150  
 CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC 3200  
 AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCTCCT GTCTTCCAT 3250  
 TCCTTATCAT GGATGTGAAC TCTTGATTG GATTTCTCAG ACCAGCAAAA 3300  
 GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGCCTGAGAA 3350  
 CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GAGTCCAGCC 3400  
 CACCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GGTCTGCACC 3450  
 CTGAGGGCCC GTGGATTCTT CTTCTCTGGAG CTCCAGGAAC CAGGCAGTGA 3500  
 GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG 3550  
 GGTGTGTCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC 3600  
 TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG 3650  
 TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCCT 3700  
 CTCACCTTCT CTTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG 3750  
 ATTCCTTCTG GGCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC 3800  
 CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC 3850  
 TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT CCTGCCACAA 3900  
 CTCCTGCCTG CTGCCCTGAC GAGAGTCATC 3930  
 ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA 3972  
 GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG 4014  
 CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC 4056  
 CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG 4098  
 AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC 4140  
 ACT CGA CAG AGG CAA CAC AGT GAG GGT TCC AGC AGC CGT GAA 4182  
 GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC 4224  
 CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT 4266  
 CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA 4308  
 GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT 4350  
 CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC 4392  
 TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC 4434  
 TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG 4476  
 CTG GGT GAT AAT CAG ATC ATG GCC AAG ACA GGC TTC CTG ATA 4518  
 ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT 4560  
 GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT 4602  
 GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG 4644  
 CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC 4686  
 AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG 4728  
 GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA 4761  
 AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC 4800  
 GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG 4850  
 GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC 4900  
 AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCTGCC TCGTGTGACA 4950  
 TGAGGCCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG 5000  
 GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA 5050  
 ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC 5100  
 AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG 5150  
 TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA 5200  
 TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG 5250  
 CAGTAAATAA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT 5300  
 CTTGCCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT 5350  
 ACCTGGATTT CTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA 5400  
 TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA 5450  
 TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC 5500  
 AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTACCT 5550  
 AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG 5600  
 GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA 5650  
 GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGGAGCTG 5700  
 ATTGTAATGA TCTTGGGTGG ATCC 5724

- (2) INFORMATION FOR SEQUENCE ID NO: 9:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 4157 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: MAGE-2 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Sub D.1

C1

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGGCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACCTCTG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCAAC	500
ACCAACCCCC	CCCCATCCC	TCAAACACCA	ACCCACCCC	CAAACCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCCTG	TACCCCTGTC	800
TCAAACCTG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGCG	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGACCCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TGAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAGAGGA	GCTGTCTGCT	CATTTCAGGG	1300
GGTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTCAACCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTGTCTTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGGCC	CTCTGGTCGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCCTCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTGAC	ATCTCTCGTT	1850
GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATGTA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCGCACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723

TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC 2765  
 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807  
 TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849  
 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT 2891  
 CCC GAG CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG 2933  
 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975  
 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC 3017  
 AGA AAT TGG CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059  
 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA 3101  
 GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143  
 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3185  
 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 3227  
 ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 3269  
 CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC 3311  
 TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG 3353  
 GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT 3395  
 GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA 3437  
 ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT 3479  
 GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT 3521  
 TTG AGA GAG GGA GAA GAG TGA 3542  
 GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 3592  
 GCACCTTCCA GGGCCCCATC CATTAGCTTC GACTGCCTCG TGTGATATGA 3642  
 GGCCCATTC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692  
 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742  
 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792  
 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842  
 TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892  
 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942  
 AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992  
 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042  
 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092  
 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGS 4142  
 CCTGGTAGTA GTGGG 4157

- (2) INFORMATION FOR SEQUENCE ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 662 base pairs
    - (B) TYPE: nucleic acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-21 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Sub  
D.1

CG

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GCGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TSAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

- (2) INFORMATION FOR SEQUENCE ID NO: 11:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 1640 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA to mRNA  
 (ix) FEATURE:  
     (A) NAME/KEY: cDNA MAGE-3  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Sub  
D

12

GCCGCGAGGG	AAGCCGGCCC	AGGCTCGGTG	AGGAGGCAAG	GTTCTGAGGG	50
GACAGGCTGA	CCTGGAGGAC	CAGAGGCCCC	CGGAGGAGCA	CTGAAGGAGA	100
AGATCTGCCA	GTGGGTCTCC	ATTGCCCAGC	TCCTGCCCAC	ACTCCCGCCT	150
GTTGCCCTGA	CCAGAGTCAT	C			171
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	213
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG	GTG GGT GCG	255
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCT	297
TCT ACT CTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	339
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	381
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	423
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	465
CCT GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	507
GTG GCC GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	549
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GGG AGT	GTC GTC	591
GGA AAT TGG	CAG TAT TTC	TTT CCT GTG	ATC TTC AGC	AAA GCT	633
TCC AGT TCC	TTG CAG CTG	GTC TTT GGC	ATC GAG CTG	ATG GAA	675
GTG GAC CCC	ATC GGC CAC	TTG TAC ATC	TTT GCC ACC	TGC CTG	717
GGC CTC TCC	TAC GAT GGC	CTG CTG GGT	GAC AAT CAG	ATC ATG	759
CCC AAG GCA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	801
AGA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	843
CTG AGT GTG	TTA GAG GTG	TTT GAG GGG	AGG GAA GAC	AGT ATG	885
TTG GGG GAT	CCC AAG AAG	CTG CTC ACC	CAA CAT TTC	GTG CAG	927
GAA AAC TAC	CTG GAG TAC	CGG CAG GTC	CCC GGC AGT	GAT CCT	969
GCA TGT TAT	GAA TTC CTG	TGG GGT CCA	AGG GCC CTC	GTT GAA	1011
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ATG GTA AAG	ATC AGT	1053
GGA GGA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAG	TGG GTT	1095
TTG AGA GAG	GGG GAA GAG	TGA			1116
GTCTGAGCAC	GAGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	1166
GCACCTTCCG	GGGCCGCATC	CCTTAGTTTC	CACAGCCTCC	TGTGACGTGA	1216
GGCCCATCT	TCACTCTTTG	AAGCGAGCAG	TCAGCATTCT	TAGTAGTGCG	1266
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTA	TTCTTTGTTT	CCTGTTGGAG	1316
TTGTTCAAAT	GTTCTTTTAA	ACGGATGGTT	GAATGAGGCT	CAGCATCCAG	1366
GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGAG	1416
TAAGAGTCTT	GttTTTTTACT	CAAATTgGGA	AATCCATTCC	ATTTTGTGAA	1466
TTGTGACATA	ATAATAGCAG	TGGTAAAAGT	ATTTGCTTAA	AATTGTGAGC	1516
GAATTAGCAA	TAACATACAT	GAGATAACTC	AAGAAATCAA	AAGATAGTTG	1566
ATTCTTGCCT	TGTACCTCAA	TCTATTCTGT	AAAATTAAAC	AAATATGCAA	1616
ACCAGGATTT	CCTTGACTTC	TTTG			1640

- (2) INFORMATION FOR SEQUENCE ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 943 base pairs
    - (B) TYPE: nucleic acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-31 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCCACTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT 50  
 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100  
 GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150  
 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGCTCA 200  
 GATAGTGCCA ACGGTGAAGG TTGCCTTGG ATTCAAACCA AGGGCCCCAC 250  
 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300  
 TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC 350  
 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC 400  
 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG 450  
 TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC 500  
 TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCCACA 550  
 CTCCCGCCTG TTGCCCTGAC CAGAGTCATC 580  
 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 622  
 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 664  
 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 706  
 TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 748  
 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 790  
 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 832  
 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 874  
 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916  
 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943



- (2) INFORMATION FOR SEQUENCE ID NO: 13:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 2531 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: MAGE-4 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50  
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100  
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150  
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200  
 TGGTCTGAGA CAGTGTCTCT AGGTTACAGA GCAGAGGATG CACAGGCTGT 250  
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300  
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350  
 CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA 400  
 CTTCTCTCCT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450  
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500  
 TAGAGCCTCT AAGATTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550  
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTGT 600  
 CCTGCTGCCC TGACCAGAGT CATC 624  
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666  
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA 708  
 CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC 750  
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792  
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834  
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876  
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC 918  
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960  
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002  
 GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC 1044  
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086  
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128  
 GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170  
 CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212  
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254  
 GCA ATG GAG GGC GAC AGC GGC TCT GAG GAG GAA ATC TGG GAG 1296  
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338  
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380  
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422  
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464  
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506  
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548  
 GCT TTG TTA GAG GAG GAA GGA GTC TGA 1578  
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628  
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678  
 CATTCTTCAC TCTGTTTGAA GAAAAATAGT AGTGTTCTTA GTAGTGGGTT 1728  
 TCTATTTTGT TGGATGACTT GGAGATTAT CTCTGTTTCC TTTTACAATT 1778  
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828  
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878  
 AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG 1928  
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT 1978  
 GAAATAGGTG AGATAAATTA AAAGATACTT AATCCCCGCC TTATGCCTCA 2028  
 GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTTTGG 2078  
 CTTCTGTAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTGA 2128  
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGGAAGGCC 2178  
 AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228  
 GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278  
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328  
 GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378  
 AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC 2428  
 AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC 2478

TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT  
GGG

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2531

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- (2) INFORMATION FOR SEQUENCE ID NO: 14:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2531 base pairs
- (B) TYPE: nucleic acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-41 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG 50  
 GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC 100  
 TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG 150  
 GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT 200  
 TGGTCTGAGA CAGTGTCTCTC AGGTACAGA GCAGAGGATG CACAGGCTGT 250  
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300  
 CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT 350  
 CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA 400  
 CTTCTCTCCT CAGGTCTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC 450  
 TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT 500  
 TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC 550  
 TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACCTTG 600  
 CCTGCTGCCC TGAGCAGAGT CATC 624  
 ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 666  
 GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG 708  
 CAG GCT CCT ACT ACT GAG GAG GAG GCT GCT GTC TCC TCC 750  
 TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT 792  
 GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT 834  
 GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC 876  
 AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC 918  
 TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC 960  
 AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA 1002  
 GCC AAG GAG CTG GTC ACA AAG GAA GAA ATG CTG GAG AGA GTC 1044  
 ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA 1086  
 GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG 1128  
 GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC 1170  
 CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC 1212  
 TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT 1254  
 GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG 1296  
 GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT 1338  
 GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG 1380  
 CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT 1422  
 CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT 1464  
 GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC 1506  
 AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA 1548  
 GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA 1578  
 GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC 1628  
 ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC 1678  
 CATTCTTCAC TCTGTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT 1728  
 TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT 1778  
 GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT 1828  
 TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG 1878  
 AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG 1928  
 GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT 1978  
 GAAATAGGTG AGATAAATTA AAAGATACTT AATTCGCCCTT TATGCCTCA 2028  
 GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTCTGG 2078  
 CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTGA 2128  
 ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC 2178  
 AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA 2228  
 GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT 2278  
 CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT 2328  
 GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA 2378  
 AACTCCATTT TCTTCTGAGG GATCTGATTG TAATGAAGCT TGGTGGGTCC 2428

AGGGCCAGAT TCTGAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC  
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT  
GGG

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## (2) INFORMATION FOR SEQUENCE ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1068 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

## (ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 40  
 GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 82  
 CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 124  
 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 166  
 GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 208  
 GGC ATT GAC GTG AAG GAA GTG GAG CCC GCC AGC AAC ACC TAC 250  
 ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 292  
 GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 334  
 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 376  
 GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 418  
 GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 460  
 ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 502  
 GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT 544  
 CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG 586  
 CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA 628  
 TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC 670  
 TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGACAG 720  
 TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG 770  
 GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG 820  
 GTTTCTATTT TGTGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA 870  
 ATTGTTGAAA GTTTCCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA 920  
 AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT 970  
 AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT 1020  
 TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC 1068

- (2) INFORMATION FOR SEQUENCE ID NO: 16:  
 (i) SEQUENCE CHARACTERISTICS:  
   (A) LENGTH: 2226 base pairs  
   (B) TYPE: nucleic acid  
   (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
   (A) NAME/KEY: MAGE-5 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50  
 GGGACCATTG ACCCCAAGAG GGTGGAGACC TCACAGATTG CAGCCTACCC 100  
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150  
 GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT 200  
 TGGTCTGAGG CCGTGCCCTC AGGTACAGAG GCAGAGGAGA TGCAGACGTC 250  
 TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300  
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350  
 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT 400  
 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450  
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500  
 ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550  
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600  
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644  
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 684  
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 728  
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 770  
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 812  
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 854  
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 896  
 TGG CTG ACT TGA 908  
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA 958  
 GAAATGCTCG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1008  
 CTTCCGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA 1058  
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1108  
 CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG 1158  
 GCCTCCTGAT AATCGTCTTG GGCATGATTC CAATGGAGGG CAAATGCGTC 1208  
 CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG 1258  
 GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT 1308  
 TGGTGCAGGA AAATACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC 1358  
 ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA 1408  
 CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATT CTACCCATC 1458  
 CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG 1508  
 CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG 1558  
 CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC 1608  
 TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGT TCTGTTCTAT 1658  
 TGGATGACTT TGAGATTGT CTTTGTTTCC TTTTGAAT GTTCAAATGT 1708  
 TTCTTTTAAT GGGTGGTTGA ATGAACCTCA GCATTCAAAT TTATGAATGA 1758  
 CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT 1808  
 TTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAAT GGGACATAGT 1858  
 TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAC 1908  
 TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC 1958  
 TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCTTGGC 2008  
 TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT 2058  
 TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTGCTC TGTGGAAGGC 2108  
 CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA 2158  
 CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT 2208  
 GCCCTCTAAG ATGTAGAG 2226

- (2) INFORMATION FOR SEQUENCE ID NO: 17:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 2305 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: MAGE-51 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG 50  
 GGGACCATT CACCAAGAG GGTGGAGACC TCACAGATT CAGCCTACCC 100  
 TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG 150  
 GGCCCATGCA TTCTCTTCC AGGAGCTCCA GGAACAGAC ACTGAGGCCT 200  
 TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC 250  
 TAGTGCCAGC AGTGACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC 300  
 GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG 350  
 TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT 400  
 CTCACCTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG 450  
 GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG 500  
 ATCTGTAAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA 550  
 GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC 600  
 AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 644  
 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 686  
 GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC 728  
 AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT 770  
 CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG 812  
 GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA 854  
 TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA 896  
 AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC 938  
 CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG 980  
 TGG CTG ACT TGA 992  
 TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA 1042  
 GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT 1092  
 CTTGCGCAAA GCCTCCGAGT CCTTGAGCT GGTCTTTGGC ATTGACGTGA 1142  
 AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA 1192  
 CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC 1242  
 CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGCAAAAT GCGTCCCTGA 1292  
 GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG 1342  
 AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTACCCA AGATTGGTG 1392  
 CAGGAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC 1442  
 TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGA AGTACTGGAG 1492  
 CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCCTACC CATCCCTGCA 1542  
 TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG 1592  
 CCAGGGCCAC TGCAGGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT 1642  
 CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCAT CTCTCTCTT 1692  
 TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG 1742  
 ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCTTTT 1792  
 TAATGGGTGG TTGAATGAAC TTCAGCATT AAATTATGA ATGACAGTAG 1842  
 TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA 1892  
 TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC 1942  
 AGTGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAAGTATGA 1992  
 GATAAAGAAA TTAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC 2042  
 GGTAATAATT TTTTAAATA ATGTGCATAC CTGGATTTC TTGGCTTCTT 2092  
 TGAGAAATGA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT 2142  
 GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG 2192  
 GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG 2242  
 TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT 2292  
 CTAAGATGTA GAG 2305

- (2) INFORMATION FOR SEQUENCE ID NO: 18:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 225 base pairs  
    (B) TYPE: nucleic acid  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(ix) FEATURE:  
    (A) NAME/KEY: MAGE-6 gene  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42  
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84  
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126  
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168  
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210  
TGT GCC CCT GAG GAG 225

Seq  
D1



- (2) INFORMATION FOR SEQUENCE ID NO: 19:  
 (i) SEQUENCE CHARACTERISTICS:  
   (A) LENGTH: 1947 base pairs  
   (B) TYPE: nucleic acid  
   (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
   (A) NAME/KEY: MAGE-7 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA 50  
 GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC 100  
 TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA 150  
 GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC 200  
 ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT 250  
 GGTTCACAAA TGAGGCCCCC CACAAGCTCC TTCTCTCCCC AGATCTGTGG 300  
 GTTCCTCCCC ATCGCGCAGC TGCTGCCCCG ACTCCAGCCT GCTGCCCTGA 350  
 CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG 400  
 GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCAGCAG 450  
 GCTCCCGCCA CCGAGGAGGA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA 500  
 AGGCACCCGT GAGGAGGTGG CTGCTGCTGG GTCCCCAGT CCTCCCCTGA 550  
 GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA 600  
 GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC 650  
 TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA 685  
 ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT 727  
 ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA 769  
 GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT 811  
 GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC 853  
 ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA 895  
 CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC 937  
 AGA GCA TGC CCG AGA CCG GCC TTC TGA 964  
 TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG 1014  
 GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT 1064  
 TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC 1114  
 TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT 1164  
 CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG 1214  
 AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG 1264  
 CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC 1314  
 AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTT 1364  
 CACACATCCA CCACCTTCCC TGTCTGTGTA CATGAGGCCG ATTCTTCACT 1414  
 CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG 1464  
 GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTGGGC 1514  
 GATTTGGAGG TTTATCTTTG TTTCTTTTGG CAGTCGTTCA AATGTTTCCTT 1564  
 TTAATGGATG GTGTAATGAA CTTCAACATT CATTTTCATGT ATGACAGTAG 1614  
 GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT 1664  
 TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG 1714  
 CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAAATGG 1764  
 GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCAGG 1814  
 CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA 1864  
 GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA 1914  
 AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG 1947

- (2) INFORMATION FOR SEQUENCE ID NO: 20:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 1810 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: MAGE-8 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG AACGAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA 50  
 TCACAGAGCA TAAGAGGCCG AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT 100  
 GTTTCCCCTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA 150  
 ACCCCACAGT TCCTGGGCTT ACCAGCCCTT TTGTCACTCC TGGAGCCTTG 200  
 GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA 250  
 GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA 300  
 CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA 350  
 CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT 400  
 CAATTGCCCA GCTCCGGCCC AACTCTCCT GCTGCCCTGA CCTGAGTCAT 450  
 C 451  
 ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA 493  
 GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG 535  
 CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC 577  
 TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT 619  
 GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT 661  
 TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT 703  
 GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC 745  
 CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT 787  
 GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA 829  
 TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG 871  
 AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC 913  
 AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT 955  
 GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC 997  
 ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT 1039  
 CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC 1081  
 ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC 1123  
 TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA 1156  
 TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG 1206  
 AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT 1256  
 CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG 1306  
 CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA 1356  
 TTTCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT 1406  
 TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG 1456  
 GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTCCCT GCTCTGTTAC 1506  
 ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA 1556  
 GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC 1606  
 AGTTCTCTGT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG 1656  
 AATTGTTCCA ATGTTCTTTC TAATGGATGG TGTAATGAAC TTCAACATTC 1706  
 ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA 1756  
 GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA 1806  
 ATTC 1810

- (2) INFORMATION FOR SEQUENCE ID NO: 21:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 1412 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: MAGE-9 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC 50  
 AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT 100  
 GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCTACTG 150  
 TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC 200  
 TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA 250  
 GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT 300  
 TGTTAGAACC TCCAAGGTTT GGTCTCAGC TGAAGTCTCT CACACACTCC 350  
 CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC 400  
 CTGACTGCTG CCCTGACCAG AGTCATC 427  
 ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA 469  
 GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA 511  
 CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT 553  
 GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT 595  
 CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC 637  
 GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC 679  
 AGT CAA GAA GAG GAA GAG CCA AGC TCC TGG GTC GAC CCA GCT 721  
 CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG 763  
 GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG 805  
 GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA 847  
 AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC 889  
 GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG 931  
 GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GGT CTT GGC 973  
 CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC 1015  
 AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC GTA ACC 1057  
 AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG 1099  
 AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC 1141  
 GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA 1183  
 AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG 1225  
 CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC 1267  
 AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA 1309  
 AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG 1351  
 GGA GAG GAG CAA GAG GGA GTC TGA 1375  
 GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA 1412

- (x) INFORMATION FOR SEQUENCE ID NO: 22:  
 (i) SEQUENCE CHARACTERISTICS:  
   (A) LENGTH: 920 base pairs  
   (B) TYPE: nucleic acid  
   (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
   (A) NAME/KEY: MAGE-10 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Sub  
D-1

1  
C

ACCTGCTCCA	GGACAAAGTG	GACCCCACTG	CATCAGCTCC	ACCTACCCTA	50
CTGTCACTCC	TGGAGCCTTG	GCCTCTGCCG	GCTGCATCCT	GAGGAGCCAT	100
CTCTCACTTC	CTTCTTCAGG	TTCTCAGGGG	ACAGGGAGAG	CAAGAGGTCA	150
AGAGCTGTGG	GACACCACAG	AGCAGCACTG	AAGGAGAAGA	CCTGTAAGTT	200
GGCCTTTGTT	AGAACCTCCA	GGGTGTGGTT	CTCAGCTGTG	GCCACTTACA	250
CCCTCCCTCT	CTCCCCAGGC	CTGTGGGTCC	CCATCGCCCA	AGTCCTGCCC	300
ACACTCCAC	CTGCTACCCT	GATCAGAGTC	ATC		333
ATG CCT CGA	GCT CCA AAG	CGT CAG CGC	TGC ATG CCT	GAA GAA	375
GAT CTT CAA	TCC CAA AGT	GAG ACA CAG	GGC CTC GAG	GGT GCA	417
CAG GCT CCC	CTG GCT GTG	GAG GAG GAT	GCT TCA TCA	TCC ACT	459
TCC ACC AGC	TCC TCT TTT	CCA TCC TCT	TTT CCC TCC	TCC TCC	501
TCT TCC TCC	TCC TCC TGC	TAT CCT CTA	ATA CCA AGC	ACC	543
CCA GAG GAG	GTT TCT GCT	GAT GAT GAG	ACA CCA AAT	CCT CCC	585
CAG AGT GCT	CAG ATA GCC	TGC TCC TCC	CCC TCG GTC	GTT GCT	627
TCC CTT CCA	TTA GAT CAA	TCT GAT GAG	GGC TCC AGC	AGC CAA	669
AAG GAG GAG	AGT CCA AGC	ACC CTA CAG	GTC CTG CCA	GAC AGT	711
GAG TCT TTA	CCC AGA AGT	GAG ATA GAT	GAA AAG GTG	ACT GAT	753
TTG GTG CAG	TTT CTG CTC	TTC AAG TAT	CAA ATG AAG	GAG CCG	795
ATC ACA AAG	GCA GAA ATA	CTG GAG AGT	GTC ATA AAA	AAT TAT	837
GAA GAC CAC	TTC CCT TTG	TTG TTT AGT	GAA GCC TCC	GAG TGC	879
ATG CTG CTG	GTC TTT GGC	ATT GAT GTA	AAG GAA GTG	GAT CC	920

- (2) INFORMATION FOR SEQUENCE ID NO: 23:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 1107 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: MAGE-11 gene  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Sub D.7

AGAGAACAGG	CCAACCTGGA	GGACAGGAGT	CCCAGGAGAA	CCCAGAGGAT	50
CACTGGAGGA	GAACAAQTGT	AAGTAGGCCT	TTGTTAGATT	CTCCATGGTT	100
CATATCTCAT	CTGAGTCTGT	TCTCACGCTC	CCTCTCTCCC	CAGGCTGTGG	150
GGCCCCATCA	CCCAGATATT	TCCCACAGTT	CGGCCTGCTG	ACCTAACCAG	200
AGTCATCATG	CCTCTTGAGC	AAAGAAGTCA	GCACTGCAAG	CCTGAGGAAG	250
CCTTCAGGCC	CAAGAAGAAG	ACCTGGGCCT	GGTGGGTGCA	CAGGCTCTCC	300
AAGCTGAGGA	GCAGGAGGCT	GCCTTCTTCT	CCTCTACTCT	GAATGTGGGC	350
ACTCTAGAGG	AGTTGCCTGC	TGCTGAGTCA	CCAAGTCCTC	CCCAGAGTCC	400
TCAGGAAGAG	TCCTTCTCTC	CCAATGCCAT	GGATGCCATC	TTTGGGAGCC	450
TATCTGATGA	GGGCTCTGGC	AGCCAAGAAA	AGGAGGGGCC	AAGTACCTCG	500
CCTGACCTGA	TAGACCCTGA	GTCCTTTTCC	CAAGATATAC	TACATGACAA	550
GATAATTGAT	TTGGTTCATT	TATTCTCCGC	AAGTATCGAG	TCAAGGGGCT	600
GATCACAAG	GCAGAA				616
ATG CTG GGG	AGT GTC ATC AAA	AAT TAT GAG GAC	TAC TTT CCT		658
GAG ATA TTT	AGG GAA GCC TCT	GTA TGC ATG CAA	CTG CTC TTT		700
GGC ATT GAT	GTG AAG GAA GTG	GAC CCC ACT AGC	CAC TCC TAT		742
GTC CTT GTC	ACC TCC CTC AAC	CTC TCT TAT GAT	GGC ATA CAG		784
TGT AAT GAG	CAG AGC ATG CCC	AAG TCT GGC CTC	CTG ATA ATA		826
GTC CTG GGT	GTA ATC TTC ATG	GAG GGG AAC TGC	ATC CCT GAA		868
GAG GTT ATG	TGG GAA GTC CTG	AGC ATT ATG GGG	GTG TAT GCT		910
GGA AGG GAG	CAC TTC CTC TTT	GGG GAG CCC AAG	AGG CTC CTT		952
ACC CAA AAT	TGG GTG CAG GAA	AAG TAC CTG GTG	TAC CGG CAG		994
GTG CCC GGC	ACT GAT CCT GCA	TGC TAT GAG TTC	CTG TGG GGT		1036
CCA AGG GCC	CAC GCT GAG ACC	AGC AAG ATG AAA	GTT CTT GAG		1078
TAC ATA GCC	AAT GCC AAT GGG	AGG GAT CC			1107

- (2) INFORMATION FOR SEQUENCE ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2150 base pairs
- (B) TYPE: nucleic acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: smage-I
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Sub 24

TCTGTCTGCA	TATGCCTCCA	CTTGTGTGTA	GCAGTCTCAA	ATGGATCTCT	50
CTCTACAGAC	CTCTGTCTGT	GTCTGGCACC	CTAAGTGGCT	TTGCATGGGC	100
ACAGGTTTCT	GCCCCCTGCAT	GGAGCTTAAA	TAGATCTTTC	TCCACAGGCC	150
TATACCCCTG	CATTGTAAGT	TTAAGTGGCT	TTATGTGGAT	ACAGGTCTCT	200
GCCCTTGAT	GCAGGCCTAA	GTTTTTCTGT	CTGCTTAACC	CCTCCAAGTG	250
AAGCTAGTGA	AAGATCTAAC	CCACTTTTGG	AAGTCTGAAA	CTAGACTTTT	300
ATGCAGTGGC	CTAACAAGTT	TTAATTTCTT	CCACAGGGTT	TGCAGAAAAG	350
AGCTTGATCC	ACGAGTTTCA	AAGTCCTGGT	ATGTTCTAG	AAAG	394
ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT					436
CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT					478
TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT					520
ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG					565
AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG					604
GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT					646
TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT					688
TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA					730
GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT					772
GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA					814
GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG					856
AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG					898
ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT					940
AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA					982
ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG					1024
GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA					1066
CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG					1108
TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC					1150
TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA					1192
TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG					1234
ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG					1276
GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC					1314
CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA					1360
ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT					1402
GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT					1444
CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA					1486
GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT					1528
AAC ATG TAG					1537
TTGAGTCTGT	TCTGTTGTGT	TTGAAAAACA	GTCAGGCTCC	TAATCAGTAG	1587
AGAGTTTATA	GCCTACCAGA	ACCAACATGC	ATCCATTCTT	GGCCTGTTAT	1637
ACATTAGTAG	AATGGAGGCT	ATTTTGTGTA	CTTTTCAAAT	GTTTGTTTAA	1687
CTAAACAGTG	CTTTTGGCCA	TGCTTCTTGT	TAAGTGCATA	AAGAGGTAAC	1737
TGTCATTGT	CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTGATG	GCAATGTGAT	ATCATAACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG	TCT				2150

- (2) INFORMATION FOR SEQUENCE ID NO: 25:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 2099 base pairs  
     (B) TYPE: nucleic acid  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: genomic DNA  
 (ix) FEATURE:  
     (A) NAME/KEY: smage-II  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Sub D7

ACCTTATTGG	GCTGTCTGTC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCCCTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCACTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTGAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAAG	TGAAAGAAGC	AGTTACAAGG	AGTGAATGAG	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCTC	ATTTGCTGGT	AGGCAAACCTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAG	AGGTCTCCTA	ATGTCGTGCC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCTGTGG	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAGTCC	TGGAAGTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCACT	1450
TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
AAGGGTGTTC	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
GAGTCTGTTC	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAAGTG	1750
TCACTTGTC	GATTAGGACT	TGTTTTGTGA	TTTGCAACAA	ACTGGAAAAC	1800
ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTGTGATGA	2000
CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACCTCTA	TTACTTTATT	2050
ATTTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

- (2) INFORMATION FOR SEQUENCE ID NO: 26:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acids
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr

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